

**AMENDMENTS TO THE CLAIMS:**

Please amend the claims as follows:

1. (Currently Amended) ~~A method to isolate at least one target molecule of a compound comprising a functional group that can be specifically altered, said method comprises the following steps:~~

~~(a) — adding said compound to a complex mixture of molecules wherein said compound stably interacts with at least one molecule forming a compound-target complex,~~

~~(b) — separating the resulting complex mixture of molecules and compound-target complexes into fractions via chromatography,~~

~~(c) — chemically, or enzymatically, or chemically and enzymatically altering said compound present on at least one compound-target complex in each fraction, and~~

~~(d) — isolating at least one target molecule that interacts with said compound via chromatography, wherein the chromatography of steps (b) and (d) is performed with the same type of chromatography~~

A method to isolate at least one target molecule of a compound, said compound comprising a functional group that can be chemically, or enzymatically, or chemically and enzymatically altered such that an altered compound-target molecule complex migrates differently from its unaltered version in the same chromatographic separation, said method comprising the following steps:

(a) adding said compound to a complex mixture of molecules wherein said compound stably interacts with at least one of said molecules forming a compound-target molecule complex,

(b) separating the resulting complex mixture of molecules and compound-target molecule complexes into multiple fractions in a first chromatographic step wherein in a fraction derived from said chromatographic step both molecules and compound-target molecule complexes are found,

(c) chemically, or enzymatically, or chemically and enzymatically altering said compound present in at least one compound-target molecule complex in each fraction, and

(d) isolating at least one target molecule that interacts with said compound in a second chromatographic step, wherein the chromatography of steps (b) and (d) is performed with the same or substantially similar type of chromatography

2. (Currently Amended) The method of claim 1, wherein said complex mixture of molecules is a complex mixture of proteins~~the chromatographic conditions of steps (b) and (d) are the same or substantially similar.~~

3. (Currently Amended) A method according to claim 2 further comprising the cleavage of said complex protein mixture into a protein peptide mixture before performing step (b)~~claims 1 wherein said complex mixture of molecules is a complex mixture of proteins.~~

4. (Currently Amended) A method according to claim 1 wherein said complex mixture of molecules is a protein peptide mixture~~claim 3 further comprising the cleavage of said complex protein mixture into a protein peptide mixture before performing step (b).~~

5. (Currently Amended) A method according to any one of claims 1 to 4 further comprising the step of identifying the targets~~claims 1 wherein said complex mixture of molecules is a protein peptide mixture.~~

6. (Currently Amended) The method of claim 5, wherein said target molecules are proteins or peptides and wherein said identifying step is performed by a method selected from the group consisting of: a tandem mass spectrometric method and/or Post-Source Decay analysis and/or measurement of the mass of the peptides, in combination with peptide and protein sequence database searching~~1, further comprising the step of identifying the targets.~~

7. (Currently Amended) The method of claim 6, wherein the measurement of the mass of the peptides in the identifying step is further combined with one or more of the following: (a) the determination of the number of free amino groups in the target peptides, (b) the cleavage specificity of the protease used to generate the protein peptide mixture; and (c) the grand average of the hydropathicity of the target peptides~~wherein said target molecules are proteins or peptides and wherein said identifying step is performed by a method selected from the group consisting of: a~~

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~~tandem mass spectrometric method, Post-Source Decay analysis, measurement of the  
mass of the peptides, in combination with database searching.~~

Claims 8-12. (Canceled)